

# NutraHacker

Fitness Injury Report for Customer: 84adea33-9194-4753-925f-529a87656048

## Instructions:

This report analyzes polymorphisms that have been found to influence activity with bones, ligaments, tendons and injuries.

PEP - Performance Enhancing Polymorphism

When one PEP allele is written, each allele provides a benefit, when two are listed then both alleles have to be present for the benefit.

NOTICE: NutraHacker reports are for scientific, educational and nutritional information only and are not intended to diagnose, cure, treat or prevent any disease, disorder or condition. Consult your doctor before beginning any treatment.

Thank you for using NutraHacker. To your health!

Gender of customer: Male

| rsID   | Gene   | Variant | PEP | Your Genotype | Genotype Freq | Category                 | Publication Highlights  |
|--|--------|---------|-----|---------------|---------------|--------------------------|---|
| rs1800012  | COL1A1 | G1245T  | AA  | CC            | 64.8727%      | tendon, ligament, injury | The major constituent of tendons is type 1 collagen which is encoded by COL1A1 gene |
| COL1A1 rs1800012 polymorphism may be associated with the reduced risk of sports-related tendon or ligament injuries, especially in ACL injuries, and that rare TT may played as a protective role. |        |         |     |               |               |                          |   |
| TT protective of ACL rupture.  |        |         |     |               |               |                          |   |
| G may be more prone to ligament injury   |        |         |     |               |               |                          |   |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/28206959">https://www.ncbi.nlm.nih.gov/pubmed/28206959</a>  |        |         |     |               |               |                          |   |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/19193663">https://www.ncbi.nlm.nih.gov/pubmed/19193663</a>  |        |         |     |               |               |                          |   |

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|---|--------|---------|-----|---------------|---------------|--------------------------|--|
| rs1107946   | COL1A1 | G-1997T | AA  | CC            | 53.7395%      | tendon, ligament, injury | Scars develop at the end of the natural wound-healing process and are characterized by excessive collagen deposition, particularly types I and III collagen. |
| The incidence of COL1A1 (rs1107946) genotype GG was significantly associated with a risk of scars.      |        |         |     |               |               |                          |  |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/27511505">https://www.ncbi.nlm.nih.gov/pubmed/27511505</a> |        |         |     |               |               |                          |  |

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|--|--------|---------|-----|---------------|---------------|--------------------------|---|
| rs3196378  | COL5A1 | N/A     | A   | AC            | 46.7168%      | tendon, ligament, injury | Fibrillar collagen, associates with collagen type 1 |
| The TC inferred haplotype (rs12722, rs3196378) was found to be overrepresented (global p = 0.008) in the South African tendinopathy group compared with all other haplotypes |        |         |     |               |               |                          |   |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/18443036">https://www.ncbi.nlm.nih.gov/pubmed/18443036</a>  |        |         |     |               |               |                          |   |

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| rs12722  | COL5A1 | BstUI<br>C414T | T   | CT            | 44.0276%      | flexibility, sprinting performance | Collagens have a triple-helical domain as their common structural element. The COL5A1 gene (location: 9q34.2-q34.3) encodes the pro-alpha-1 chain of type V collagen, the rate-limiting component of the of type V collagen trimer assembly. Heterotypic collagen I/V interactions are believed to regulate the fibril diameter and fibril number in vitro (Wenstrup et al., 2004). |
| <p>The COL5A1 gene rs12722 C/T polymorphism has recently been shown to be associated with passive straight leg raise and/or a sit-and-reach measurement (the carriers of the rs12722 T allele were more inflexible) (Brown et al., 2011b; Collins et al., 2009). Since data suggest that inflexibility improves running performance, possibly through enhancing the storage and return of energy and minimizing the need for muscle-stabilizing activity (Craib et al., 1996), it was hypothesized that the rs12722 T allele would associate with improved running performance. Indeed, in a study of 313 Caucasian Ironman triathletes Posthumus et al. (2011) has shown that participants with a TT genotype completed the running component (42.2-km) of the race significantly faster than individuals with a CC genotype (TT: 294.2 ± 52.1 min, CC: 307.4 ± 48.6 min; P = 0.019).</p> |        |                |     |               |               |                                    |   |
| <p>Since data suggest that inflexibility improves running performance, possibly through enhancing the storage and return of energy and minimizing the need for muscle-stabilizing activity (Craib et al., 1996), it was hypothesized that the rs12722 T allele would associate with improved running performance. Indeed, in a study of 313 Caucasian Ironman triathletes Posthumus et al. (2011) has shown that participants with a TT genotype completed the running component (42.2-km) of the race significantly faster than individuals with a CC genotype (TT: 294.2 ± 52.1 min, CC: 307.4 ± 48.6 min; P = 0.019).</p>   |        |                |     |               |               |                                    |   |
| <p>This study suggested the possibility that tendon structures of individuals with a COL5A1 rs12722 CC genotype were more extensible than individuals with other genotypes (combined TT and CT).</p>   |        |                |     |               |               |                                    |   |
| <p><a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3728528/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3728528/</a></p>   |        |                |     |               |               |                                    |   |

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|--|--------|----------------|-----|---------------|---------------|--------------------------|--|
| rs13946  | COL5A1 | DpnII<br>C230T | C   | N/A           | N/A           | tendon, ligament, injury | Individuals within both populations with a CC genotype for the BstUI RFLP had a significantly decreased risk of developing tendinopathy versus any other genotypes (Australian odds ratio 0.42, 95% CI 0.20 to 0.86, p = 0.017). |
| <p><a href="https://www.ncbi.nlm.nih.gov/pubmed/18443036">https://www.ncbi.nlm.nih.gov/pubmed/18443036</a></p> |        |                |     |               |               |                          |  |

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|---|--------|-----------------|-----|---------------|---------------|--------------------------|---|
| rs35796750  | COL6A1 | IVS32-29<br>T/C | TT  | N/A           | N/A           | ligament,<br>performance | alpha1 chain of type V and type VI collagen - extracellular matrix (ECM) structural component of musculoskeletal soft tissue - known mutations involved in various clinical muscle diseases (cause hyperelasticity in the muscles -> decreased function) - biomechanics: stiffer connective tissue (inflexibility) -> enhanced storage/return of energy -> increased running economy -> increased endurance performance |
| rs35796750: intron 32, T/C, T= ancestral allele - CC genotype (vs CT + TT) associated with multiple muscle diseases - TT genotype (vs CT + CC) associated with increased endurance performance (faster Ironman Triathlon finish time) [p=0.030] |        |                 |     |               |               |                          |   |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/22012643">https://www.ncbi.nlm.nih.gov/pubmed/22012643</a>   |        |                 |     |               |               |                          |   |

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|--|-------|---------|-----|---------------|---------------|-----------------|---------------------------------------|
| rs679620   | MMP-3 | N/A     | T   | CT            | 48.5561%      | tendon strength | Degrades collagens and other proteins |
| The MMP3 rs679620 GG genotype was found to be overrepresented in the Achilles tendon rupture (RUP) group (AA, 24.0%; AG, 32.0%; GG, 44.0%) compared to controls (AA, 26.7%; AG, 54.2%; GG, 19.1%). |       |         |     |               |               |                 |                                       |
| The rs1800796 of IL-6 and rs679620 of MMP-3 were found significantly associated with increased susceptibility and severity of post-operative stiffness.  |       |         |     |               |               |                 |                                       |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/27222816">https://www.ncbi.nlm.nih.gov/pubmed/27222816</a>  |       |         |     |               |               |                 |                                       |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/26191285">https://www.ncbi.nlm.nih.gov/pubmed/26191285</a>  |       |         |     |               |               |                 |                                       |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/19042922">https://www.ncbi.nlm.nih.gov/pubmed/19042922</a>  |       |         |     |               |               |                 |                                       |

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|--|-------|---------|-----|---------------|---------------|-----------------|---------------------------------------|
| rs650108   | MMP-3 | N/A     | G   | N/A           | N/A           | tendon strength | Degrades collagens and other proteins |
| rs650108 SNP of MMP-3 were associated with increased risk of post-operative stiffness susceptibility and severity. This finding can be used in guiding the rehabilitation procedure after rotator cuff surgery, in another word, those with the genetic susceptibility factors should receive a more radical rehabilitation procedure and those without the susceptibility factors can be more conservative. |       |         |     |               |               |                 |                                       |
| <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4503156/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4503156/</a>  |       |         |     |               |               |                 |                                       |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/27211292">https://www.ncbi.nlm.nih.gov/pubmed/27211292</a>  |       |         |     |               |               |                 |                                       |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/19042922">https://www.ncbi.nlm.nih.gov/pubmed/19042922</a>  |       |         |     |               |               |                 |                                       |

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|---|--------|---------|-----|---------------|---------------|---------------------|---|
| rs2228059   | ILR15A | N/A     | A   | N/A           | N/A           | bone, muscle volume | The IL-15 receptor alpha (IL-15R-alpha) is a part of the trimeric plasma membrane receptor for the pleiotropic cytokine IL-15 (Giri et al., 1995) that affects parameters associated with skeletal muscle fibre hypertrophy (Quinn et al., 1995). |
| The presence of the A allele in the exon 3 of the IL15RA gene (Asn146Thr, rs2228059 A/C) was associated with greater whole muscle volume and greater baseline cortical bone volumes.  |        |         |     |               |               |                     |   |
| Although there were no significant differences in genotype distributions between elite endurance athletes and sprint athletes, it was shown that this SNP was associated with endurance athlete status in specific sports, such as cycling (n = 73) had a greater percentage of the A allele, while triathletes (n = 13) and elite rowers (n = 26) had a greater percentage of the C allele compared to controls. |        |         |     |               |               |                     |   |
| When analyzing SNPs in the IL-15R-alpha gene, the presence of the C-allele of the 3rd exon in the rs2228059 IL-15R-alpha SNP was associated with lesser values for serum triglycerides in males   |        |         |     |               |               |                     |   |
| The presence of the A-allele in the 3rd exon of the rs2228059 IL-15R-alpha SNP was associated with greater whole muscle volume (Figure 3A) but lower muscle quality measured at baseline in males (Figure 3B).  |        |         |     |               |               |                     |   |
| Additionally, the A-allele in the 3'UTR of the rs2296135 IL-15R-alpha SNP was associated with a greater baseline total bone volume in females (Figure 3E). The A-allele in the 3rd exon of the rs2228059 IL-15R-alpha SNP was associated with greater baseline cortical bone volumes in females (Figure 3F)   |        |         |     |               |               |                     |   |
| <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2593832/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2593832/</a> , <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2593832/figure/F3/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2593832/figure/F3/</a>   |        |         |     |               |               |                     |   |

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|--|--------|---------|-----|---------------|---------------|---------------------|---|
| rs2296135  | ILR15A | N/A     | A   | AC            | 49.103%       | bone, muscle volume | The IL-15 receptor alpha (IL-15R-alpha) is a part of the trimeric plasma membrane receptor for the pleiotropic cytokine IL-15 (Giri et al., 1995) that affects parameters associated with skeletal muscle fibre hypertrophy (Quinn et al., 1995). |
| The C allele in the 3'UTR of the IL15RA gene (rs2296135 C/A) was associated with greater improvements in post-training isometric strength, while A allele was associated with a greater baseline total bone volume   |        |         |     |               |               |                     |   |
| In a study of 76 men and 77 women who completed 10-week total body high activity resistance training, the carriage of the A allele (rs2296135 C/A) was strongly associated with muscle hypertrophy, although those with the greatest hypertrophy had lower muscle strength and muscle quality increases (Riechman et al., 2004). |        |         |     |               |               |                     |   |
| The C-allele in the 3'UTR of the rs2296135 IL-15R-alpha SNP was associated with greater improvements in post-training isometric strength in females (Figure 3C).   |        |         |     |               |               |                     |   |
| Additionally, the A-allele in the 3'UTR of the rs2296135 IL-15R-alpha SNP was associated with a greater baseline total bone volume in females (Figure 3E).   |        |         |     |               |               |                     |   |
| <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2593832/figure/F3/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2593832/figure/F3/</a>  |        |         |     |               |               |                     |   |
| <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2593832/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2593832/</a>  |        |         |     |               |               |                     |   |

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|--|------|---------|-----|---------------|---------------|-------------------|--|
| rs2073711  | CILP | T1184C  | A   | AG            | 44.794%       | ligament strength | Meta-analysis to collect all eligible studies for investigating whether cartilage intermediate layer protein (CILP) gene rs2073711 polymorphism is associated with susceptibility to intervertebral disc degeneration (IVD). |
| Meta-analysis found that the CILP 2073711 polymorphism was significantly associated with IVD risk. The estimated OR of risk allele T of rs2073711 was 1.36. (95% CI=1.18-1.55, P<0.001). |      |         |     |               |               |                   |  |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/27359356">https://www.ncbi.nlm.nih.gov/pubmed/27359356</a>  |      |         |     |               |               |                   |  |

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|---|------|---------|-----|---------------|---------------|----------|---|
| rs10735810  | VDR  | fokI/f  | A   | N/A           | N/A           | bone     | The VDR is involved in sustaining normocalcemia by inhibiting the production of parathyroid hormone and has effects on bone and skeletal muscle biology (Hausler et al., 2011; Garfia et al., 2002). Vdr knockout mice develop a low bone mass phenotype with hypocalcemia, hypophosphatemia and elevated calcitriol levels (Yoshizawa et al., 1997). |
| The C allele (also called F allele – absence of the endonuclease FokI restriction site) carriers have a 3-amino acid shorter VDR than do individuals with the T allele (or f allele – presence of the FokI restriction site). The shorter VDR has enhanced transactivation capacity as a transcription factor (Whitfield et al., 2001). Rabon-Stith et al. (2005) studied VDR genotypes of 206 healthy men and women (50-81 years old) before and after either aerobic exercise training or strength training. VDR FokI genotype was significantly related to the femoral neck bone mineral density in response to strength training, but not aerobic training. More specifically, the heterozygotes (TC) in the strength training group approached a significantly greater increase in femoral neck bone mineral density compared to TT homozygotes. |      |         |     |               |               |          |   |
| Homozygous TT genotype of the VDR gene was significantly more represented in young soccer players than in a matched sedentary population.   |      |         |     |               |               |          |   |
| Boys with the TC genotype had higher total body bone mineral content and density compared to those with CC genotype. It was suggested that effect of the FokI polymorphism on bone mineralization occurs during bone maturation, possibly at the initial pubertal stages.   |      |         |     |               |               |          |   |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/27797588">https://www.ncbi.nlm.nih.gov/pubmed/27797588</a>   |      |         |     |               |               |          |   |

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|---|------|---------|-----|---------------|---------------|----------|---|
| rs699947  | VEGF | A2578C  | A   | N/A           | N/A           | ligament | The VEGFA rs699947 CC genotype (p=0.010, OR: 1.92, 95% CI: 1.17-3.17) was significantly over-represented within participants with non-contact ACL ruptures. |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/25111568">https://www.ncbi.nlm.nih.gov/pubmed/25111568</a> |      |         |     |               |               |          |   |

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|---|------|---------|-----|---------------|---------------|----------|---|
| rs1570360   | VEGF | N/A     | GG  | AG            | 43.5991%      | ligament | The VEGFA rs1570360 GA genotype was significantly over-represented in the CON group (p=0.007, OR: 1.70, 95% CI: 1.16-2.50). |
| Association with Achilles tendinopathy  |      |         |     |               |               |          |   |
| <a href="https://www.ncbi.nlm.nih.gov/pubmed/25111568">https://www.ncbi.nlm.nih.gov/pubmed/25111568</a> |      |         |     |               |               |          |   |